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RAW SEQUENCE LISTING DATE: 01/11/2001
 PATENT APPLICATION: US/09/746,390 TIME: 16:55:59

Input Set : A:\Gfb5.app
 Output Set: N:\CRF3\01112001\I746390.raw

ENTERED

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Jens Kossmann
 6 Ruth Lorberth
 8 (ii) TITLE OF INVENTION: PLANTS WHICH SYNTHESIZE A MODIFIED STARCH,
 9 PROCESS FOR THE PRODUCTION THEREOF AND MODIFIED STARCH

12 (iii) NUMBER OF SEQUENCES: 4

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: FISH & NEAVE
 16 (B) STREET: 1251 Avenue of the Americas
 17 (C) CITY: New York
 18 (D) STATE: New York
 19 (E) COUNTRY: USA
 20 (F) ZIP: 10020

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/746,390
 C--> 30 (B) FILING DATE: 21-Dec-2000
 C--> 31 (C) CLASSIFICATION:

41 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: PCT/EP96/04109
 35 (B) FILING DATE: 19-SEP-1996
 38 (A) APPLICATION NUMBER: DE 19547733.2
 39 (B) FILING DATE: 20-DEC-1995
 42 (A) APPLICATION NUMBER: DE 19534759.5
 43 (B) FILING DATE: 19-SEP-1995

45 (viii) ATTORNEY/AGENT INFORMATION:

46 (A) NAME: Haley Jr., James F.
 47 (B) REGISTRATION NUMBER: 27,794
 48 (C) REFERENCE/DOCKET NUMBER: GFB-5

50 (ix) TELECOMMUNICATION INFORMATION:

51 (A) TELEPHONE: 212-596-9000
 52 (B) TELEFAX: 212-596-9090

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 4856 base pairs
 58 (B) TYPE: nucleotide
 59 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear

62 (ii) MOLECULE TYPE: cDNA to mRNA

64 (vi) ORIGINAL SOURCE:

65 (A) ORGANISM: Solanum tuberosum
 66 (B) STRAIN: C.V. Berolina

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68      (ix) FEATURE:
69          (A) NAME/KEY: CDS
70          (B) LOCATION:105..4497
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72      CATCTTCATC GAATTTCCTG AAGCTTCCTC GCTAATTTC TGGTTTCITC ACICAAAATC      60
73      GACGTTTCTA GCTCAACTTC AGTGAATIAA GCCACTGGGA GGAT ATG AGT AAT ICC      116
74                                          Met Ser Asn Ser
75                                          1
81      TTA GGG AAT AAC TGG CTG TAC CAG GGA TTC CTA ACC TCA ACA GTG TGG      164
82      Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu
83      5      10      15      20
85      GAA CAT AAA AGT AGA ATC AGT CCT CCT TGT GTT GGA GGC AAT TCT TIG      212
86      Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu
87      25      30      35
88      TTT CAA CAA CAA GTG ATC TCG AAA TCA CCT TTA TCA ACT GAG TTT CGA      260
89      Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser Thr Glu Phe Arg
90      40      45      50
92      GGT AAC AGG TTA AAG GTG CAG AAA AAG AAA ATA CCT ATG GAA AAG AAG      308
93      Gly Asn Arg Leu Lys Val Gln Lys Lys Lys Ile Pro Met Glu Lys Lys
94      55      60      65
96      CGT GCT TTT TCT AGT TCT CCT CAT GCT GTA CTT ACC ACT GAT ACC TCT      356
97      Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser
98      70      75      80
100     ICT GAG CTA GCA GAA AAG TTC AGT CTA GGG GGG AAT ATT GAG CTA CAG      404
101     Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn Ile Glu Leu Gln
102     85      90      95      100
104     GTT GAT GTT AGG CCT CCC ACT TCA GGT GAT GTG TCC TTT GTG GAT TTT      452
105     Val Asp Val Arg Pro Thr Ser Gly Asp Val Ser Phe Val Asp Phe
106     105      110      115
108     CAA GTA ACA AAT GGT AGT GAT AAA CTG TTT TTG CAC TGG GGG GCA GTA      500
109     Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His Trp Gly Ala Val
110     120      125      130
112     AAA TTC GGG AAA GAA ACA TGG TCT CTT CCG AAT GAT CGT CCA GAT GGG      548
113     Lys Phe Gly Lys Gln Thr Trp Ser Leu Pro Asn Asp Arg Pro Asp Gly
114     135      140      145
116     ACC AAA GTG TAC AAG AAC AAA CCA CTT AGA ACT CCA TTT GTT AAA TCT      596
117     Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro Phe Val Lys Ser
118     150      155      160
120     GGC TCT AAC TCC ATC CTG AGA CTG GAG ATA CGA GAC ACT GCT ATC GAA      644
121     Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp Thr Ala Ile Glu
122     165      170      175      180
124     GCT ATT GAG TTT CTC ATA TAC GAT GAA GCC CAC GAT AAA TGG ATA AAG      692
125     Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp Lys Trp Ile Lys
126     185      190      195
128     AAT AAT GGT GGT AAT TTT CGT GTC AAA TTG TCA AGA AAA GAG ATA CGA      740
129     Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg Lys Glu Ile Arg
130     200      205      210
132     GGC CCA GAT GTT TCT GTT CCT GAG GAG CTT GTA CAG ATC CAA TCA TAT      788
133     Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln Ile Gln Ser Tyr

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| | | | | |
|---|-----|-----|-----|------|
| 134 | 215 | 220 | 225 | |
| 137 TTG AGG TGG CAG AGG AAG GCA AAA CAG AAT TAC CCC CCT GAG AAA GAG | | | | 836 |
| 138 Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro Pro Glu Lys Glu | | | | |
| 139 230 | 235 | 240 | | |
| 141 AAG GAG GAA TAT GAG GCT GCT CGA ACT GTC CTA CAG GAG GAA ATA GCI | | | | 884 |
| 142 Lys Glu Glu Lys Glu Ala Ala Arg Thr Val Leu Gln Glu Glu Ile Ala | | | | |
| 143 245 | 250 | 255 | 260 | |
| 145 CGT GGT GCT TCC ATA CAG GAC ATT CGA GCA AGG CTA ACA AAA ACT AAT | | | | 932 |
| 146 Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu Thr Lys Thr Asn | | | | |
| 147 265 | 270 | 275 | | |
| 148 GAT AAA AGT CAA AGC AAA GAA CAG CCT CTT CAT GTA ACA AAG AGT GAT | | | | 980 |
| 149 Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val Thr Lys Ser Asp | | | | |
| 150 280 | 285 | 290 | | |
| 152 ATA CCT GAT GAC CTT GCC CAA GCA CAA GCT TAC ATT AGG TCG CAG AAA | | | | 1028 |
| 153 Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile Arg Trp Glu Lys | | | | |
| 154 295 | 300 | 305 | | |
| 156 GCA GGA AAG CCG AAC TAT CCT CCA GAA AAG CAA ATT GAA GAA CTC GAA | | | | 1076 |
| 157 Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile Glu Glu Leu Glu | | | | |
| 158 310 | 315 | 320 | | |
| 160 GAA GCA AGA AGA GAA TTG CAA CTT GAG CTT GAG AAA GGC ATT ACC CTT | | | | 1124 |
| 161 Glu Ala Arg Arg Glu Leu Glu Leu Glu Lys Gly Ile Thr Leu | | | | |
| 162 325 | 330 | 335 | 340 | |
| 164 GAT GAG TTG CGG AAA ACG ATT ACA AAA GGG GAG ATA AAA ACT AAG GTG | | | | 1172 |
| 165 Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile Lys Thr Lys Val | | | | |
| 166 345 | 350 | 355 | | |
| 168 GAA AAG CAC CTG AAA AGA AGT TCT TTT GCC GTT GAA AGA ATC CAA AGA | | | | 1220 |
| 169 Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu Arg Ile Gln Arg | | | | |
| 170 360 | 365 | 370 | | |
| 172 AAG AAG AGA GAC TTT GGG CAT CTT ATT AAT AAG TAT ACT TCC AGT CCT | | | | 1268 |
| 173 Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr Thr Ser Ser Pro | | | | |
| 174 375 | 380 | 385 | | |
| 176 GCA GTA CAA GTA CAA AAG GTC TTG GAA GAA CCA CCA GCC TTA TCT AAA | | | | 1316 |
| 177 Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro Ala Leu Ser Lys | | | | |
| 178 390 | 395 | 400 | | |
| 180 ATT AAG CTG TAT GC. AAG GAG AAG GAG GAG CAG ATT GAT GAT CCG ATC | | | | 1364 |
| 181 Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile Asp Asp Pro Ile | | | | |
| 182 405 | 410 | 415 | 420 | |
| 184 CTA AAT AAA AAG ATC TTT AAG GTC GAT GAT GGG GAG CTA CTG GTA CTG | | | | 1412 |
| 185 Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu Leu Leu Val Leu | | | | |
| 186 425 | 430 | 435 | | |
| 188 GTA GCA AAG TCC TCT GGG AAG ACA AAA GTA CAT CTA GCT ACA GAT CTG | | | | 1460 |
| 189 Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu Ala Thr Asp Leu | | | | |
| 190 440 | 445 | 450 | | |
| 192 AAT CAG CCA ATT ACT CTT CAC TGG GCA TTA TCC AAA AGT CCT GGA GAG | | | | 1508 |
| 193 Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Pro Gly Glu | | | | |
| 194 455 | 460 | 465 | | |
| 196 TGG ATG GTA CCA CCT TCA AGC ATA TTG CCT CCT GGG TCA ATT ATT TTA | | | | 1556 |
| 197 Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu | | | | |
| 198 470 | 475 | 480 | | |

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| | | |
|-----|---|------|
| 200 | GAC AAG GCT GCC GAA ACA CCT TTT TCA GCC AGT TCT TCT GAT GGT CTA | 1604 |
| 201 | Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Ser Asp Gly Leu | |
| 202 | 485 490 495 500 | |
| 204 | ACT TCT AAG GTA CAA TCT TGG GAT ATA CTA ATT GAA GAT GGC AAT TTT | 1652 |
| 205 | Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe | |
| 206 | 505 510 515 | |
| 208 | GIG GGG ATG CCA TTT GAT CTT TIG TCT GGT GAA AAA TGG ATT AAG AAC | 1700 |
| 209 | Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Ile Lys Asn | |
| 210 | 520 525 530 | |
| 212 | CAA GGG TCG GAT TTC TAT GGT GGC TTC AGT GGT GCA TCC AAA TTA GCA | 1748 |
| 213 | Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala Ser Lys Leu Ala | |
| 214 | 535 540 545 | |
| 216 | CTC AAG GCT GCT GGG GAT GGC ACT GGA ACT GCA AAG TCT TTA CTG GAT | 1796 |
| 217 | Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp | |
| 218 | 550 555 560 | |
| 220 | AAA ATA GCA GAT ATG GAA AGT GAG GCT CAG AAG TCA TTT ATG CAC CGG | 1844 |
| 221 | Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg | |
| 222 | 565 570 575 580 | |
| 224 | TTT AAT ATT GCA GCT GAC TTG ATA GAA GAT GCC ACT AGT GCT GGT GAA | 1892 |
| 225 | Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu | |
| 226 | 585 590 595 | |
| 228 | CTT GGT TTT GCT GGA ATT CTT GTA TGG ATG AGG TTC ATG GCT ACA AGG | 1940 |
| 229 | Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg | |
| 230 | 600 605 610 | |
| 232 | CAA CTG ATA TGG AAC AAA AAC TAT AAC GTA AAA CCA CGT GAA ATA AGC | 1988 |
| 233 | Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser | |
| 234 | 615 620 625 | |
| 236 | AAG GCT CAG GAC AGA CTT ACA GAC TTG TTG CAG AAT GCT TTC ACC AGT | 2036 |
| 237 | Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser | |
| 238 | 630 635 640 | |
| 240 | CAC CCT CAG TAC CGT GAA ATT TTG CGG ATG ATT ATG TCA ACT GTT GCA | 2084 |
| 241 | His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly | |
| 242 | 645 650 655 660 | |
| 245 | CGT CGA GGT GAA GGG GAT GTA GCA CAG CGA ATT AGG GAT GAA ATT TIG | 2132 |
| 246 | Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu | |
| 247 | 665 670 675 | |
| 249 | GTC ATC CAG AGG AAC AAT GAC TGC AAG GGT GCT ATG ATG CAA GAA TGG | 2180 |
| 250 | Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met Met Gln Glu Trp | |
| 251 | 680 685 690 | |
| 253 | CAT CAG AAA TTG CAT AAT AAT ACT AGT CCT GAT GAT GTT GTG ATC TGT | 2228 |
| 254 | His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys | |
| 255 | 695 700 705 | |
| 257 | CAG GCA TTA ATT GAC TAC ATC AAG AGT GAT TTT GAT CTT GGT GTT TAT | 2276 |
| 258 | Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr | |
| 259 | 710 715 720 | |
| 261 | TGG AAA ACC CTG AAT GAG AAC GGA ATA ACA AAA GAG CGT CTT TTG AGT | 2324 |
| 262 | Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser | |
| 263 | 725 730 735 740 | |
| 265 | TAT GAC CGT GCT ATC CAT TCT GAA CCA AAT TTT AGA GGA GAT CAA AAG | 2372 |

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Input Set : A:\Gfb5.app

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| | | |
|-----|---|------|
| 266 | Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys | |
| 267 | 745 750 755 | |
| 268 | GGT GGT CTT TTG CGT GAT TTA GGT CAC TAT ATG AGA ACA TTG AAG GCA | 2420 |
| 269 | Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala | |
| 270 | 760 765 770 | |
| 272 | CTT CAT TCA GGT CCA GAT CTT GAG TCT GCT ATT GCA AAC TCC ATG GGC | 2468 |
| 273 | Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly | |
| 274 | 775 780 785 | |
| 276 | TAC AAA ACT GAG GGA GAA GGC TTT ATG GTT GGA GTC CAG ATA AAT CCT | 2516 |
| 277 | Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro | |
| 278 | 790 795 800 | |
| 280 | GTA TCA GGC TTG CCA TCT GGC TTT CAG GAC CTC CTC CAT TTT GTC TTA | 2564 |
| 281 | Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu His Phe Val Leu | |
| 282 | 805 810 815 820 | |
| 284 | GAC CAT GTG GAA GAT AAA AAT GTG GAA ACT CTT CTT GAG AGA TTG CTA | 2612 |
| 285 | Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Arg Leu Leu | |
| 286 | 825 830 835 | |
| 288 | GAG GCT CGT GAG GAG CTT AGC CCC TTG CTT CTC AAA CCA AAC AAC CCT | 2660 |
| 289 | Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys Pro Asn Asn Arg | |
| 290 | 840 845 850 | |
| 292 | CTA AAG GAT CTG CTG TTT TTG GAC ATA GCA CTT GAT TCT ACA GTT AGA | 2708 |
| 293 | Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg | |
| 294 | 855 860 865 | |
| 296 | ACA GCA GTA GAA AGG GGA TAT GAA GAA TTG AAC AAC GCT AAT CCT GAG | 2756 |
| 297 | Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu | |
| 298 | 870 875 880 | |
| 300 | AAA ATC ATG TAC TTC ATC TCC CTC GTT CTT GAA AAT CTC GCA CTC TCT | 2804 |
| 301 | Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser | |
| 302 | 885 890 895 900 | |
| 304 | GTG GAC GAT AAT GAA GAT CTT GTT TAT TGC TTG AAG GGA TGG AAT CAA | 2852 |
| 305 | Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln | |
| 306 | 905 910 915 | |
| 308 | GCT CTT TCA ATG TCC AAT GGT GGG GAC AAC CAT TGG GCT TTA TTT GCA | 2900 |
| 309 | Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala | |
| 310 | 920 925 930 | |
| 312 | AAA GCT GTG CTT GAC AGA ACC CGT CTT GCA CTT GCA AGC AAG GCA GAG | 2948 |
| 313 | Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala Ser Lys Ala Glu | |
| 314 | 935 940 945 | |
| 316 | TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA TCA ATA | 2996 |
| 317 | Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile | |
| 318 | 950 955 960 | |
| 320 | CTT GGG GTG GAC CAA TGG CCT TTG AAC ATA TTT ACT GAA GAA ATT ATA | 3044 |
| 321 | Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile | |
| 322 | 965 970 975 980 | |
| 324 | CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA CTC GAT | 3092 |
| 325 | Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp | |
| 326 | 985 990 995 | |
| 328 | CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT ATC AGT | 3140 |
| 329 | Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser | |

VERIFICATION SUMMARY

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Output Set: N:\CRF3\01112001\I746390.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:31 M:220 C: Keyword misspelled or invalid format, [(C) CLASSIFICATION:]
L:415 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 1
L:897 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 3